

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223966
Seq. ID LIB3165-060-Q1-K1-F11
Method BLASTX
NCBI GI g3763916
BLAST score 331
E value 6.0e-31
Match length 126
% identity 53

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]
>gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown
protein [Arabidopsis thaliana]

Seq. No. 223967
Seq. ID LIB3165-060-Q1-K1-F12
Method BLASTX
NCBI GI g729668
BLAST score 242
E value 1.0e-20
Match length 55
% identity 84

NCBI Description HISTONE H1 >gi_2147479_pir_S65059 histone H1,
drought-inducible - Lycopersicon pennellii >gi_436823
(U01890) Solanum pennellii histone H1 [Solanum pennellii]

Seq. No. 223968
Seq. ID LIB3165-060-Q1-K1-F3
Method BLASTX
NCBI GI g1352821
BLAST score 352
E value 1.0e-33
Match length 67
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
(RUBISCO SMALL SUBUNIT) >gi_279581_pir_RKCNSU
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 223969
Seq. ID LIB3165-060-Q1-K1-F5
Method BLASTX
NCBI GI g4455223
BLAST score 403
E value 2.0e-39
Match length 126
% identity 32

NCBI Description (AL035440) putative DNA binding protein [Arabidopsis
thaliana]

Seq. No. 223970
Seq. ID LIB3165-060-Q1-K1-F6


```
Seq. ID      LIB3166-001-Q1-K1-C1
Method       BLASTX
NCBI GI      g3790567
BLAST score   196
E value      4.0e-15
Match length  116
% identity    36
NCBI Description (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
thaliana]
```

Seq. No.	224001
Seq. ID	LIB3166-001-Q1-K1-C11
Method	BLASTX
NCBI GI	g1495804
BLAST score	631
E value	4.0e-66
Match length	137
% identity	86
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

```
Seq. No.          224002
Seq. ID          LIB3166-001-Q1-K1-C12
Method           BLASTX
NCBI GI          g1170504
BLAST score       175
E value          1.0e-12
Match length      68
% identity        49
NCBI Description  EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82
                  (IEIF-(ISO)4F P82) >gi_452440 (M95747) initiation factor
                  (iso)4f p82 subunit [Triticum aestivum]
```

Seq. No.	224003
Seq. ID	LIB3166-001-Q1-K1-C2
Method	BLASTX
NCBI GI	g4455340
BLAST score	235
E value	1.0e-19
Match length	65
% identity	68
NCBI Description	(AL035522) putative protein [Arabidopsis thaliana]

```
Seq. No.      224004
Seq. ID      LIB3166-001-Q1-K1-C3
Method       BLASTX
NCBI GI      g1408471
BLAST score   511
E value      5.0e-52
Match length  113
% identity    81
NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]
```

Seq. No.	224005
Seq. ID	LIB3166-001-Q1-K1-C6
Method	BLASTX

NCBI GI g3021355
 BLAST score 409
 E value 5.0e-40
 Match length 89
 % identity 88
 NCBI Description (AJ005081) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No. 224006
 Seq. ID LIB3166-001-Q1-K1-C7
 Method BLASTX
 NCBI GI g2829918
 BLAST score 548
 E value 2.0e-56
 Match length 129
 % identity 81
 NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No. 224007
 Seq. ID LIB3166-001-Q1-K1-C8
 Method BLASTX
 NCBI GI g4314378
 BLAST score 343
 E value 3.0e-32
 Match length 136
 % identity 51
 NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 224008
 Seq. ID LIB3166-001-Q1-K1-D10
 Method BLASTX
 NCBI GI g4263712
 BLAST score 408
 E value 6.0e-40
 Match length 98
 % identity 77
 NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis thaliana]

Seq. No. 224009
 Seq. ID LIB3166-001-Q1-K1-D11
 Method BLASTX
 NCBI GI g1706482
 BLAST score 169
 E value 6.0e-12
 Match length 107
 % identity 40
 NCBI Description DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
 >gi_860937_emb_CAA58467_(X83441) DNA ligase IV [Homo sapiens] >gi_4504997_ref_NP_002303.1_pLIG4_ligase IV, DNA, ATP-dependent

Seq. No. 224010
 Seq. ID LIB3166-001-Q1-K1-D3
 Method BLASTX
 NCBI GI g2459429

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

```
Seq. No.      224026
Seq. ID      LIB3166-001-Q1-K1-G3
Method       BLASTX
NCBI GI      g2780194
BLAST score   546
E value      4.0e-56
Match length  123
% identity    58
NCBI Description (AJ003197) adenine nucleotide translocator [Lupinus albus]
```

Seq. No.	224027
Seq. ID	LIB3166-001-Q1-K1-G5
Method	BLASTX
NCBI GI	g4262250
BLAST score	370
E value	2.0e-35
Match length	108
% identity	74
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	224028
Seq. ID	LIB3166-001-Q1-K1-G6
Method	BLASTX
NCBI GI	g3859116
BLAST score	360
E value	2.0e-34
Match length	120
% identity	59
NCBI Description	(AF031609) unknown [Oryza sativa]

Seq. No.	224029
Seq. ID	LIB3166-001-Q1-K1-G8
Method	BLASTX
NCBI GI	g1946369
BLAST score	142
E-value	9.0e-09
Match length	84
% identity	44
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

```
Seq. No.      224030
Seq. ID      LIB3166-001-Q1-K1-G9
Method       BLASTX
NCBI GI      g1346769
BLAST score   501
E value      8.0e-51
Match length  136
% identity    65
NCBI Description  PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
>gi_558596_emb_CAA52605_1(X74496) prolyl oligopeptidase
[Homo sapiens]>gi_1585155_prf_2124300A Pro oligopeptidase
[Homo sapiens]>gi_4506043_ref_NP_002717.1_pPREP_prolyl
endopeptidase
```

Seq. No.	224031
Seq. ID	LIB3166-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g3402704
BLAST score	344
E value	2.0e-32
Match length	119
% identity	66
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224032
Seq. ID	LIB3166-001-Q1-K1-H4
Method	BLASTX
NCBI GI	g421836
BLAST score	603
E value	8.0e-63
Match length	139
% identity	84
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]
Seq. No.	224033
Seq. ID	LIB3166-001-Q1-K1-H5
Method	BLASTX
NCBI GI	g2252631
BLAST score	158
E value	1.0e-10
Match length	63
% identity	49
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224034
Seq. ID	LIB3166-001-Q1-K1-H6
Method	BLASTX
NCBI GI	g3319342
BLAST score	164
E value	2.0e-11
Match length	45
% identity	64
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]
Seq. No.	224035
Seq. ID	LIB3166-001-Q1-K1-H7
Method	BLASTX
NCBI GI	g1352076
BLAST score	162
E value	4.0e-11
Match length	134
% identity	33
NCBI Description	BETA-GALACTOSIDASE (LACTASE) >gi_144746 (M35107) beta-D-galactosidase (cbgA) [Clostridium acetobutylicum]
Seq. No.	224036
Seq. ID	LIB3166-001-Q1-K1-H8
Method	BLASTX


```
Seq. No.      224047
Seq. ID      LIB3166-001-Q1-K3-B7
Method       BLASTX
NCBI GI      g886116
BLAST score   481
E value      1.0e-48
Match length  124
% identity    69
NCBI Description (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
              (AF051338) xyloglucan endotransglycosylase related protein
              [Arabidopsis thaliana]
```

Seq. No.	224048
Seq. ID	LIB3166-001-Q1-K3-B9
Method	BLASTX
NCBI GI	g2829918
BLAST score	511
E value	4.0e-52
Match length	121
% identity	80
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	224049
Seq. ID	LIB3166-001-Q1-K3-C1
Method	BLASTX
NCBI GI	g1545805
BLAST score	159
E value	5.0e-11
Match length	89
% identity	48
NCBI Description	(D64052) cytochrome P450 like TBP [Nicotiana tabacum]

Seq. No.	224050
Seq. ID	LIB3166-001-Q1-K3-C11
Method	BLASTX
NCBI GI	g4262225
BLAST score	304
E value	6.0e-28
Match length	108
% identity	51
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

```
Seq. No.      224051
Seq. ID       LIB3166-001-Q1-K3-C2
Method        BLASTX
NCBI GI       g2459429
BLAST score    461
E value       3.0e-46
Match length   116
% identity     73
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
```

Seq. No.	224052
Seq. ID	LIB3166-001-Q1-K3-C3
Method	BLASTX

NCBI GI	g4249410
BLAST score	519
E value	5.0e-53
Match length	119
% identity	81
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

```
Seq. No.      224053
Seq. ID       LIB3166-001-Q1-K3-C4
Method        BLASTX
NCBI GI       g3402704
BLAST score    312
E value       1.0e-28
Match length  107
% identity    67
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      224054
Seq. ID      LIB3166-001-Q1-K3-C7
Method       BLASTX
NCBI GI      g2501572
BLAST score   387
E value      2.0e-37
Match length  107
% identity    63
NCBI Description  LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
                (L47118) EMB8 gene product [Picea glauca]
```

Seq. No.	224055
Seq. ID	LIB3166-001-Q1-K3-D1
Method	BLASTX
NCBI GI	g4206789
BLAST score	517
E value	7.0e-53
Match length	123
% identity	82
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	224056
Seq. ID	LIB3166-001-Q1-K3-D3
Method	BLASTX
NCBI GI	g3281848
BLAST score	164
E value	2.0e-11
Match length	113
% identity	46
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	224057
Seq. ID	LIB3166-001-Q1-K3-D7
Method	BLASTX
NCBI GI	g4204313
BLAST score	414
E value	9.0e-41
Match length	91
% identity	85

Match length 93
 % identity 55
 NCBI Description (AF024625) arm repeat containing protein [Brassica napus]

Seq. No. 224074
 Seq. ID LIB3166-002-Q1-K1-A7
 Method BLASTX
 NCBI GI g4105782
 BLAST score 293
 E value 2.0e-26
 Match length 67
 % identity 87
 NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 224075
 Seq. ID LIB3166-002-Q1-K1-A8
 Method BLASTX
 NCBI GI g3461846
 BLAST score 372
 E value 1.0e-35
 Match length 108
 % identity 30
 NCBI Description (AC005315) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No. 224076
 Seq. ID LIB3166-002-Q1-K1-A9
 Method BLASTX
 NCBI GI g1762428
 BLAST score 356
 E value 8.0e-34
 Match length 94
 % identity 68
 NCBI Description (U59467) aromatic rich glycoprotein JP630 [Arabidopsis thaliana]

Seq. No. 224077
 Seq. ID LIB3166-002-Q1-K1-B1
 Method BLASTX
 NCBI GI g3688123
 BLAST score 395
 E value 2.0e-38
 Match length 120
 % identity 66
 NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No. 224078
 Seq. ID LIB3166-002-Q1-K1-B10
 Method BLASTX
 NCBI GI g418507
 BLAST score 167
 E value 1.0e-11
 Match length 71
 % identity 48
 NCBI Description S-ADENOSYLMETHIONINE:2-DEMETHYLMENAQUINONE METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical


```
BLAST score      299
E value         4.0e-27
Match length    82
% identity      76
NCBI Description (AC002392) putative serine proteinase [Arabidopsis thaliana]
```

```
Seq. No.      224135
Seq. ID      LIB3166-003-P1-K1-C12
Method       BLASTX
NCBI GI      g1174162
BLAST score   638
E value      7.0e-67
Match length  121
% identity    93
NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis
thaliana] >gi_3746915 (AF091106) E2
ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
```

```
Seq. No.          224136
Seq. ID           LIB3166-003-P1-K1-C2
Method            BLASTX
NCBI GI           g4218011
BLAST score       518
E value           8.0e-53
Match length      130
% identity        75
NCBI Description   (AC006135) putative protein kinase [Arabidopsis thaliana]
                  >gi_4309721_gb_AAD15491_ (AC006439) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
```

Seq. No.	224137
Seq. ID	LIB3166-003-P1-K1-C4
Method	BLASTX
NCBI GI	g3600031
BLAST score	226
E value	1.0e-18
Match length	111
% identity	51
NCBI Description	(AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No.	224138
Seq. ID	LIB3166-003-P1-K1-C9
Method	BLASTX
NCBI GI	g2244734
BLAST score	710
E value	2.0e-75
Match length	142
% identity	99
NCBI Description	(D88414) actin [Gossypium hirsutum]

```
Seq. No.      224139
Seq. ID      LIB3166-003-P1-K1-D10
Method       BLASTX
NCBI GI      g3122049
BLAST score  206
```



```
% identity      64
NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
```

```
Seq. No.      224252
Seq. ID      LIB3166-006-P1-K1-C12
Method       BLASTX
NCBI GI      g1345787
BLAST score   678
E value      1.0e-71
```

```
% identity      94
NCBI Description CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)
                  >gi_567937_dbj_BAA05641_ (D26594) chalcone synthase
                  [Camellia sinensis]
```

Seq. No.	224253
Seq. ID	LIB3166-006-P1-K1-C4
Method	BLASTX
NCBI GI	g2244732
BLAST score	446
E value	2.0e-44
Match length	90
% identity	94
NCBI Description	(D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No.	224254
Seq. ID	LIB3166-006-P1-K1-C5
Method	BLASTX
NCBI GI	g2979551
BLAST score	174
E value	9.0e-13
Match length	57
% identity	65
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]

```

Seq. No.      224255
Seq. ID       LIB3166-006-P1-K1-C7
Method        BLASTX
NCBI GI       gl28190
BLAST score    530
E value       2.0e-54
Match length   122
% identity     80
NCBI Description  NITRATE REDUCTASE 2 (NR2) >gi_66205_pir_RDNTNS nitrate
reductase (NADH) (EC 1.6.6.1) nia-2 - common tobacco
>gi_19891_emb_CAA32217_ (X14059) nitrate reductase
[Nicotiana tabacum]

```

```
Seq. No.          224256
Seq. ID           LIB3166-006-P1-K1-D1
Method            BLASTX
NCBI GI           g4490341
BLAST score       172
E value           3.0e-12
Match length      124
% identity        39
```



```
% identity      43
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
```

```
Seq. No.      224299
Seq. ID      LIB3166-007-P1-K1-C7
Method       BLASTX
NCBI GI      g1418331
BLAST score   195
E value      6.0e-15
Match length  102
% identity    39
NCBI Description (X95909) receptor like protein kinase [Arabidopsis
thaliana]
```

[illegible]

Seq. No.	224301
Seq. ID	LIB3166-007-P1-K1-C9
Method	BLASTX
NCBI GI	g4210451
BLAST score	163
E value	5.0e-19
Match length	71
% identity	76
NCBI Description	(AB016472) ARR2 protein [Arabidopsis thaliana]

```
Seq. No.      224302
Seq. ID       LIB3166-007-P1-K1-D1
Method        BLASTX
NCBI GI       g120669
BLAST score   564
E value       3.0e-58
Match length  113
% identity    94
NCBI Description  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
>gi_66014_pir_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]
```

```
Seq. No.      224303
Seq. ID      LIB3166-007-P1-K1-D10
Method       BLASTX
NCBI GI      g541818
BLAST score   490
E value      1.0e-49
```


Seq. ID	LIB3166-008-P1-K1-G4
Method	BLASTX
NCBI GI	g2224733
BLAST score	171
E value	4.0e-12
Match length	91
% identity	51
NCBI Description	(AB004933) Aux22e [<i>Vigna radiata</i>]

Seq. No.	224366
Seq. ID	LIB3166-008-P1-K1-G7
Method	BLASTX
NCBI GI	g1220196
BLAST score	279
E value	8.0e-31
Match length	104
% identity	70
NCBI Description	(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

```
Seq. No.      224367
Seq. ID      LIB3166-008-P1-K1-G9
Method       BLASTX
NCBI GI      g4220538
BLAST score   416
E value      5.0e-41
Match length  101
% identity   80
NCBI Description (AL035356) NADPH-ferrihemoprotein reductase ATR1
               [Arabidopsis thaliana]
```

Seq. No.	224368
Seq. ID	LIB3166-008-P1-K1-H1
Method	BLASTX
NCBI GI	g4580460
BLAST score	431
E value	1.0e-42
Match length	114
% identity	79
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	224369
Seq. ID	LIB3166-008-P1-K1-H2
Method	BLASTX
NCBI GI	g3549667
BLAST score	554
E value	4.0e-57
Match length	121
% identity	87
NCBI Description	(AL031394) Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana]

```
Seq. No.      224370
Seq. ID      LIB3166-008-P1-K1-H9
Method       BLASTX
NCBI GI      g1657382
BLAST score   497
```


Table 1. Demographic characteristics of the study population	
Age (years)	65.0 (SD 10.0)
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 (SD 2.0)
Marital status	
Married	40 (80.0%)
Single	10 (20.0%)
Occupation	
Retired	40 (80.0%)
Unemployed	10 (20.0%)
Income (USD/month)	1,000 (SD 200)
Health status	
Good	40 (80.0%)
Poor	10 (20.0%)
Comorbidities	
Hypertension	30 (60.0%)
Diabetes	20 (40.0%)
Cholesterol	15 (30.0%)
Smoking status	
Smoker	10 (20.0%)
Non-smoker	40 (80.0%)
Alcohol consumption	
Regular	5 (10.0%)
Occasional	15 (30.0%)
Never	30 (60.0%)
Family size	3.0 (SD 1.0)
Living alone	5 (10.0%)
Living with family	45 (90.0%)
Health insurance	
Yes	40 (80.0%)
No	10 (20.0%)
Access to healthcare	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare satisfaction	
Satisfied	35 (70.0%)
Dissatisfied	15 (30.0%)
Healthcare access barriers	
Cost	10 (20.0%)
Distance	15 (30.0%)
Time	10 (20.0%)
Information	5 (10.0%)
Transportation	5 (10.0%)
Healthcare quality	
Good	30 (60.0%)
Poor	20 (40.0%)
Healthcare provider	
Physician	10 (20.0%)
Nurse	15 (30.0%)
Pharmacist	10 (20.0%)
Other	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	
Regular	30 (60.0%)
Irregular	20 (40.0%)
Emergency	10 (20.0%)
Preventive	5 (10.0%)
Healthcare provider satisfaction	
Satisfied	30 (60.0%)
Dissatisfied	20 (40.0%)
Healthcare provider access	
Easy	35 (70.0%)
Difficult	15 (30.0%)
Healthcare provider utilization	</

Seq. No.	224392
Seq. ID	LIB3166-009-P1-K1-F2
Method	BLASTX
NCBI GI	g541847
BLAST score	268
E value	7.0e-24
Match length	63
% identity	76
NCBI Description	alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

```

Seq. No.      224393
Seq. ID       LIB3166-009-P1-K1-F3
Method        BLASTX
NCBI GI       g1707944
BLAST score   635
E value       1.0e-66
Match length  137
% identity    93
NCBI Description  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
                  PRECURSOR 2 (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                  PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                  ADENYL TRANSFERASE) >gi_541976_pir__S41292
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                  fava bean >gi_440595_emb_CAA54260_ (X76941) ADP-glucose
                  pyrophosphorylase [Vicia faba]

```

Seq. No.	224394
Seq. ID	LIB3166-009-P1-K1-F4
Method	BLASTX
NCBI GI	g4335750
BLAST score	164
E value	7.0e-12
Match length	57
% identity	58
NCBI Description	(AC006284) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

```
Seq. No.          224395
Seq. ID           LIB3166-009-P1-K1-F7
Method            BLASTX
NCBI GI           g3023536
BLAST score       388
E value           1.0e-37
Match length      127
% identity        58
```

NCBI Description MADS BOX PROTEIN CMB1 >gi_695317 (L40404) MADS box protein
[*Dianthus caryophyllus*]

Seq. No.	224396
Seq. ID	LIB3166-009-P1-K1-F9
Method	BLASTX
NCBI GI	g1345698
BLAST score	715
E value	6.0e-76
Match length	135
% identity	99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
(CAB-151) (LHCP) >gi_99601_pir_S20917 chlorophyll
a/b-binding protein - upland cotton
>gi_452314_emb_CAA38025_(X54090) chlorophyll ab binding
protein [Gossypium hirsutum]

Seq. No.	224397
Seq. ID	LIB3166-009-P1-K1-G10
Method	BLASTX
NCBI GI	g464707
BLAST score	535
E value	6.0e-55
Match length	114
% identity	90

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana
>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana]
>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]
>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	224398
Seq. ID	LIB3166-009-P1-K1-G11
Method	BLASTX
NCBI GI	g3176726
BLAST score	409
E value	4.0e-44
Match length	124
% identity	75
NCBI Description	(AC002392) putative s thaliana]

Seq. No.	224399
Seq. ID	LIB3166-009-P1-K1-G2
Method	BLASTX
NCBI GI	g2244749
BLAST score	616


```

Method                BLASTX
NCBI GI               g4049410
BLAST score           419
E value               3.0e-41
Match length         118
% identity            66
NCBI Description      (Y10225) L-ascorbate oxidase [Cucumis melo]

Seq. No.              224437
Seq. ID              LIB3166-010-P1-K1-F6
Method               BLASTX
NCBI GI              g3885338
BLAST score          324
E value              3.0e-30
Match length         102
% identity            61
NCBI Description      (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.              224438
Seq. ID              LIB3166-010-P1-K1-F7
Method               BLASTX
NCBI GI              g116923
BLAST score          251
E value              1.0e-21
Match length         82
% identity            61
NCBI Description      COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
>gi_111414_pir__S13520 beta-COP protein - rat
>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus
norvegicus]

Seq. No.              224439
Seq. ID              LIB3166-010-P1-K1-F8
Method               BLASTX
NCBI GI              g1495804
BLAST score          657
E value              4.0e-69
Match length         142
% identity            85
NCBI Description      (X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.              224440
Seq. ID              LIB3166-010-P1-K1-G1
Method               BLASTX
NCBI GI              g1707955
BLAST score          628
E value              9.0e-66
Match length         125
% identity            92
NCBI Description      GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1
(GLUTAMATE--AMMONIA LIGASE) >gi_1134896_emb_CAA63981_
(X94320) glutamine synthetase [Vitis vinifera]

Seq. No.              224441
Seq. ID              LIB3166-010-P1-K1-G10
Method               BLASTX
NCBI GI              q2935416

```



```

Seq. No.      224507
Seq. ID      LIB3166-012-P1-K1-F10
Method       BLASTX
NCBI GI      g137475
BLAST score   729
E value      1.0e-77
Match length  139
% identity   99
NCBI Description  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
(32 KD ACCESSORY PROTEIN) (P39) >gi_89602_pir_A32123
H+-transporting ATPase (EC 3.6.1.35) polypeptide IV,
vacuolar - bovine

```

Seq. No.	224508
Seq. ID	LIB3166-012-P1-K1-F11
Method	BLASTX
NCBI GI	g2833633
BLAST score	611
E value	1.0e-63
Match length	136
% identity	81
NCBI Description	(AC003108) Unknown gene product [Homo sapiens]

```
Seq. No.      224509
Seq. ID      LIB3166-012-P1-K1-F12
Method       BLASTX
NCBI GI      g543201
BLAST score   611
E value      1.0e-63
Match length  132
% identity    84
NCBI Description collagen alpha 1(I) chain precursor - mouse (fragments)
```

```
Seq. No.      224510
Seq. ID      LIB3166-012-P1-K1-F3
Method       BLASTX
NCBI GI      g117505
BLAST score   193
E value      6.0e-15
Match length  71
% identity    56
NCBI Description  CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
                (CALBP) (CALCIUM-BINDING PROTEIN 3) (CABP3)
                >gi_627974_pir_JH0819 calreticulin precursor - rat
                >gi_55855_emb_CAA37446_ (X53363) precursor (AA -17 to 399)
                [Rattus norvegicus] >gi_488841_emb_CAA55890_ (X79327)
                calreticulin [Rattus norvegicus] >gi_1845572_dbj_BAA11345_
                (D78308) calreticulin [Rattus norvegicus]
```

Seq. No.	224511
Seq. ID	LIB3166-012-P1-K1-F4
Method	BLASTX
NCBI GI	g478811
BLAST score	232
E value	1.0e-19
Match length	74

[illegible]

NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	224526
Seq. ID	LIB3166-013-P1-K1-B9
Method	BLASTX
NCBI GI	g2522534
BLAST score	185
E value	2.0e-14
Match length	86
% identity	48

NCBI Description (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No.	224527
Seq. ID	LIB3166-013-P1-K1-C1
Method	BLASTX
NCBI GI	g3269293
BLAST score	276
E value	1.0e-24
Match length	103
% identity	57
NCBI Description	(AL030978) putative

Seq. No.	224528
Seq. ID	LIB3166-013-P1-K1-C11
Method	BLASTX
NCBI GI	g2961378
BLAST score	574
E value	2.0e-59
Match length	143
% identity	39
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	224529
Seq. ID	LIB3166-013-P1-K1-C5
Method	BLASTX
NCBI GI	g3021489
BLAST score	164
E value	2.0e-15
Match length	88
% identity	62
NCBI Description	(AJ224934) histone H2B [Lycopersicon esculentum]

```
Seq. No.          224530
Seq. ID           LIB3166-013-P1-K1-C6
Method            BLASTX
NCBI GI           g3122388
BLAST score       610
E value           1.0e-63
Match length      131
% identity        31
NCBI Description   WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40
                  repeat protein [Arabidopsis thaliana]
```

Seq. No.	224531
Seq. ID	LIB3166-013-P1-K1-C7
Method	BLASTX
NCBI GI	q4510345

E value 4.0e-30
 Match length 75
 % identity 87
 NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012)
 ribosomal protein L9 [Oryza sativa]

Seq. No. 224542
 Seq. ID LIB3166-013-P1-K1-F2
 Method BLASTX
 NCBI GI g4090533
 BLAST score 460
 E value 3.0e-46
 Match length 101
 % identity 82
 NCBI Description (U68215) ACC oxidase [Carica papaya]

Seq. No. 224543
 Seq. ID LIB3166-013-P1-K1-F6
 Method BLASTX
 NCBI GI g2146739
 BLAST score 262
 E value 8.0e-23
 Match length 118
 % identity 51
 NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No. 224544
 Seq. ID LIB3166-013-P1-K1-F7
 Method BLASTX
 NCBI GI g400976
 BLAST score 426
 E value 1.0e-48
 Match length 108
 % identity 96
 NCBI Description RAS-RELATED PROTEIN RHA1 >gi_478671_pir_S23727 GTP-binding
 protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_
 (X59152) RHA1 [Arabidopsis thaliana]
 >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein
 [Arabidopsis thaliana]

Seq. No. 224545
 Seq. ID LIB3166-013-P1-K1-F9
 Method BLASTX
 NCBI GI g1888357
 BLAST score 499
 E value 1.0e-50
 Match length 123
 % identity 76
 NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
 >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
 precursor [Arabidopsis thaliana]

Seq. No. 224546
 Seq. ID LIB3166-013-P1-K1-G10
 Method BLASTX
 NCBI GI g2673910


```
Seq. No.      224552
Seq. ID      LIB3166-013-P1-K1-G7
Method       BLASTX
NCBI GI      g629722
BLAST score   175
E value      1.0e-12
Match length  122
% identity    35
NCBI Description  finger protein pcpl - potato >gi_563623_emb_CAA57772_
(X82328) putative DNA/RNA binding protein [Solanum
tuberosum]
```

```
Seq. No.      224553
Seq. ID       LIB3166-013-P1-K1-G8
Method        BLASTX
NCBI GI       g4406787
BLAST score    388
E value        1.0e-37
Match length   102
% identity     77
NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]
```

Seq. No.	224554
Seq. ID	LIB3166-013-P1-K1-G9
Method	BLASTX
NCBI GI	g3892059
BLAST score	270
E value	1.0e-23
Match length	143
% identity	48
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

```
Seq. No.      224555
Seq. ID      LIB3166-013-P1-K1-H10
Method       BLASTX
NCBI GI      g2983778
BLAST score   164
E value      2.0e-11
Match length  116
% identity    36
NCBI Description (AE000736) hypothetical protein [Aquifex aeolicus]
```

Seq. No.	224556
Seq. ID	LIB3166-013-P1-K1-H5
Method	BLASTX
NCBI GI	g4512694
BLAST score	238
E value	6.0e-20
Match length	133
% identity	41
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]

Seq. No.	224557
Seq. ID	LIB3166-013-P1-K1-H7
Method	BLASTX
NCBI GI	g464621

NCBI GI	g3738325
BLAST score	403
E value	2.0e-39
Match length	110
% identity	71
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No.	224590
Seq. ID	LIB3166-014-P1-K1-F1
Method	BLASTX
NCBI GI	g2924777
BLAST score	376
E value	3.0e-36
Match length	130
% identity	6
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

```
Seq. No.          224591
Seq. ID           LIB3166-014-P1-K1-F10
Method            BLASTX
NCBI GI           g2662415
BLAST score       173
E value           2.0e-12
Match length      56
% identity        54
NCBI Description   (U97494) metallothionein-like protein [Prunus armeniaca]
```

```
Seq. No.      224592
Seq. ID      LIB3166-014-P1-K1-F2
Method       BLASTX
NCBI GI      g1351271
BLAST score   331
E value      6.0e-31
Match length  118
% identity    62
NCBI Description  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
>gi_1084309_pir_S52032 triose-phosphate isomerase (EC
5.3.1.1) precursor, chloroplast - spinach >gi_806312
(L36387) triosephosphate isomerase, chloroplast isozyme
[Spinacia oleracea]
```

```
Seq. No.      224593
Seq. ID      LIB3166-014-P1-K1-F3
Method       BLASTX
NCBI GI      g1814424
BLAST score   582
E value      2.0e-60
Match length  134
% identity    79
NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
```

```
Seq. No.      224594
Seq. ID      LIB3166-014-P1-K1-F8
Method       BLASTX
NCBI GI      g115484
```

```

BLAST score      555
E value          3.0e-57
Match length     108
% identity       59
NCBI Description CALMODULIN 1 >gi_71684_pir_MCPZDC calmodulin - carrot
>gi_478632_pir_S22971 calmodulin - trumpet lily
>gi_541839_pir_S40301 calmodulin - Red bryony
>gi_2129970_pir_S70768 calmodulin CAM81 - garden petunia
>gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota]
>gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium
longiflorum] >gi_169207 (M80836) calmodulin [Petunia
hybrida] >gi_308900 (L18912) calmodulin [Lilium
longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin
[Malus domestica] >gi_535444 (U13882) calmodulin [Pisum
sativum] >gi_445602_prf__1909349A calmodulin [Daucus
carota]

```

```
Seq. No.      224595
Seq. ID      LIB3166-014-P1-K1-F9
Method       BLASTX
NCBI GI      g1709930
BLAST score   359
E value      2.0e-35
Match length  94
% identity    81
NCBI Description  PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE PRECURSOR (AIR
CARBOXYLASE) (AIRC) >gi_629656_pir_S43322
phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) -
moth bean >gi_349159 (L22584) 5-aminoimidazole
ribonucleotide carboxylase [Vigna aconitifolia]
```

Seq. No.	224596
Seq. ID	LIB3166-014-P1-K1-G1
Method	BLASTX
NCBI GI	g2809251
BLAST score	152
E value	2.0e-10
Match length	34
% identity	74
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

```
Seq. No.      224597
Seq. ID       LIB3166-014-P1-K1-G10
Method        BLASTX
NCBI GI       g2245087
BLAST score    218
E value       1.0e-17
Match length   86
% identity     44
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      224598
Seq. ID      LIB3166-014-P1-K1-G5
Method       BLASTX
NCBI GI      g4127456
BLAST score   303
E value      1.0e-27
```



```
Seq. No.      224613
Seq. ID      LIB3166-015-P1-K1-B2
Method       BLASTX
NCBI GI      g132944
BLAST score   215
E value      5.0e-22
Match length  92
% identity    63
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_JQ0772 ribosomal
protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
(M32655) ribosomal protein [Arabidopsis thaliana]
```

Seq. No.	224614
Seq. ID	LIB3166-015-P1-K1-B4
Method	BLASTX
NCBI GI	g3420049
BLAST score	172
E value	3.0e-12
Match length	131
% identity	40
NCBI Description	(AC004680) putative protein phosphatase 2C [Arabidopsis thaliana]

```
Seq. No.      224615
Seq. ID      LIB3166-015-P1-K1-B5
Method       BLASTX
NCBI GI      g2191136
BLAST score   312
E value      1.0e-28
Match length  110
% identity    60
NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;
                coded for by A. thaliana cDNA T46230; coded for by A.
                thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                [Arabidopsis thaliana]
```

```
Seq. No.      224616
Seq. ID      LIB3166-015-P1-K1-C10
Method       BLASTX
NCBI GI      g3953463
BLAST score   210
E value      1.0e-16
Match length  60
% identity    60
NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]
```

```
Seq. No.      224617
Seq. ID      LIB3166-015-P1-K1-C12
Method       BLASTX
NCBI GI      g728906
BLAST score   330
E value      8.0e-31
Match length  126
% identity    55
NCBI Description  PROBABLE CALCIUM-TRANSPORTING ATPASE 5
                >gi_1077722_pir__S50669 hypothetical protein YER166w -
                yeast (Saccharomyces cerevisiae) >qi_603407 (U18922)
```